

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 01:39:36 : Search time 2215 Seconds
(without alignments)
4167.687 Million cell updates/sec

Title: US-09-895-298A-32_COPY_63_632

Perfect score: 570
Sequence: 1 atgatgaattccagctcc.....aagaagtaatccagggcc 570

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_yrt:*
22: em_gss_yun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568.4	99.7	807	12	BG184448 RST3374 A
2	565.8	99.3	777	12	BG217799 RST37513
3	554.4	97.3	691	10	AM582253 QVA-ST021
4	543.6	95.4	768	12	BG194960 RST14018
5	535.4	93.9	789	12	BG221275 RST41079
6	530	93.0	837	12	BG216071 RST35885

7	523.6	91.9	810	12	BG217267 RST36969
8	523.6	91.9	823	12	BG183902 RST2815 A
9	467.8	82.1	698	12	BF375244 QVA-ST021
10	445.4	78.1	822	12	BG219307 RST39061
11	442.2	77.6	871	12	BG198917 RST18188
12	434	76.1	2721	11	AK016573 Mus muscu
13	411.6	72.2	758	12	BG198969 RST18241
14	401.4	70.4	447	13	BG982234 CMA-CN008
15	338.8	59.4	594	10	AM469181 hc78f11.x
16	299	52.5	585	10	AM469177 hc78e12.x
17	294.8	51.7	558	9	AT799626 to74b03.x
18	286.6	50.3	855	12	BG204090 RST23484
19	268	47.0	376	12	BE849364 u88h05.Y
20	268	47.0	491	10	AM913564 ufs4e02.Y
21	251.8	44.2	508	12	BF375243 QVA-ST021
22	242.8	42.6	829	12	BG201350 RST20811
23	229.4	40.2	565	14	BQ552730 H4017607
24	219.8	38.6	307	12	BG187692 RST6558 A
25	215.4	37.8	480	9	AT697014 wc76h09.x
26	210	36.8	415	14	BQ084432 K-EST0149
27	210	36.8	482	14	BM773483 K-EST0057
28	203.6	35.7	398	14	BM773482 K-EST0057
29	202	35.4	777	9	AU138880 AUI38880
30	186.8	32.8	529	13	BM432955 1JBJ8B4.a
31	182.4	32.0	268	12	BG184955 RST3889 A
32	174.4	30.6	428	9	AT1830044 wJ58f02.x
33	168.8	29.6	846	12	BG202006 RST21353
34	165	28.9	639	14	BM978431 UT-CF-DUI
35	155.8	27.3	243	12	BG216765 RST36460
36	150	26.3	191	9	AA371314 EST83087
37	139.6	24.5	652	9	AV226010 AV226010
38	122.4	21.5	359	14	BM750790 K-EST0026
39	114.2	20.0	303	12	BG205109 RST24528
40	112	19.6	422	10	BB799999 BB799999
41	109	19.1	870	9	AJ443652 AJ443652
42	105.4	18.5	340	13	BG977333 CM1-C1003
43	103.4	18.1	598	10	AM814058 RC6-ST019
44	102	17.9	748	12	BE746094 601573466
45	102	17.9	1136	14	BQ436217 AGENCOURT

ALIGNMENTS

RESULT 1
BG184448 807 bp mRNA linear EST 21-APR-2001
LOCUS RST3374 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG184448
ACCESSION BG184448
VERSION BG184448.1 GI:13706135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
'E., Veloso,N., Klika,A., Hess,J., Colthren,K., Lo,K., Offenbacher,
'J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave. Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 499.
Location/Qualifiers

source

1. .807
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="H1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 211 a 195 c 178 g 222 t 1 others

ORIGIN

Query Match 99.7%; Score 568.4; DB 12; Length 807;
Best Local Similarity 99.8%; Pred. No. 8.4e-151;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAATTTCCAGCTCCGAGCAAGCCCTGGGCGCTCAGATGATGACTTCTTC 60
DB 85 ATGATGAATTTCCAGCTCCGAGCAAGCCCTGGGCGCTCAGATGATGACTTCTTC 144

QY 61 ATCTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCCCGCCATCACCATC 120
DB 145 ATCTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCCCGCCATCACCATC 204

QY 121 TGGAGATTGAAGCTTCAGCTGAGTGGCCCTTTTGAGGTGCTCTCTTCATTCAC 180
DB 205 TGGAGATTGAAGCTTCAGCTGAGTGGCCCTTTTGAGGTGCTCTCTTCATTCAC 264

QY 181 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGTTGTTGG 240
DB 265 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGTTGTTGG 324

QY 241 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 300
DB 325 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 384

QY 301 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 360
DB 385 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 444

QY 361 CATGAGAGATCATTAATGAGGGCAAAAGTATGTTCTGATAGAAAATGATCAAG 420
DB 445 CATGAGAGATCATTAATGAGGGCAAAAGTATGTTCTGATAGAAAATGATCAAG 504

QY 421 CTGAGAGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 480
DB 505 CTGAGAGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 564

QY 481 GAGCAACAAGGCTTTTGCATTTGGGGGAACATGATGCGAGTCTTGATCTGATCTAGA 540
DB 565 GAGCAACAAGGCTTTTGCATTTGGGGGAACATGATGCGAGTCTTGATCTGATCTAGA 624

QY 541 AGATCACTTCAAGAGTATCCAAAGGCC 570
DB 625 AGATCACTTCAAGAGTATCCAAAGGCC 654

RESULT 2
BG217799 777 bp mRNA linear EST 21-Apr-2001

LOCUS BG217799 RST37513 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG217799
ACCESSION BG217799
VERSION BG217799.1 GI:13743820
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 777)
Harrington, J. J., Sherif, B., Rundlett, S., Jackson, P. D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.

, Lerner, L., Costanzo, D., McElligott, R., Booser, S., Mays, R., Smith
, E., Veloso, N., Kliska, A., Hess, J., Cothren, K., Lo, K., Offenbacher
, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9800
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 512.
Location/Qualifiers
1. .777
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="H1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 196 a 193 c 173 g 214 t 1 others

ORIGIN

Query Match 99.3%; Score 565.8; DB 12; Length 777;
Best Local Similarity 99.5%; Pred. No. 4.6e-150;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATGAATTTCCAGCTCCGAGCAAGCCCTGGGCGCTCAGATGATGACTTCTTC 60
DB 85 ATGATGAATTTCCAGCTCCGAGCAAGCCCTGGGCGCTCAGATGATGACTTCTTC 144

QY 61 ATCTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCCCGCCATCACCATC 120
DB 145 ATCTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCCCGCCATCACCATC 204

QY 121 TGGAGATTGAAGCTTCAGCTGAGTGGCCCTTTTGAGGTGCTCTCTTCATTCAC 180
DB 205 TGGAGATTGAAGCTTCAGCTGAGTGGCCCTTTTGAGGTGCTCTCTTCATTCAC 264

QY 181 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGTTGTTGG 240
DB 265 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGTTGTTGG 324

QY 241 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 300
DB 325 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 384

QY 301 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 360
DB 385 ATCATGGAACCTTCATGGAAGTGCACCTCTTTTCAATCCACCCCTCATCTGCTCA 444

QY 361 CATGAGAGATCATTAATGAGGGCAAAAGTATGTTCTGATAGAAAATGATCAAG 420
DB 445 CATGAGAGATCATTAATGAGGGCAAAAGTATGTTCTGATAGAAAATGATCAAG 504

QY 421 CTGAGAGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 480
DB 505 CTGAGAGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 564

QY 481 GAGCAACAAGGCTTTTGCATTTGGGGGAACATGATGCGAGTCTTGATCTGATCTAGA 540
DB 565 GAGCAACAAGGCTTTTGCATTTGGGGGAACATGATGCGAGTCTTGATCTGATCTAGA 624

QY 541 AGATCACTTCAAGAGTATCCAAAGGCC 570
DB 625 AGATCACTTCAAGAGTATCCAAAGGCC 654

```

RESULT 3
AM582253
LOCUS      AM582253                691 bp    mRNA    linear    EST 16-MAR-2000
DEFINITION QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM582253
VERSION     AM582253.1  GI:7257302
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 691)
            HCGP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
TITLE      JOURNAL
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?rl=QV4&f2=QV4-ST0212-120100-075-f09&f3=2000-01-12&f4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 5
            High quality sequence stop: 667.
FEATURES
    source
        1..691
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="ST0212"
            /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the puc 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT  179 a      167 c      157 g      188 t
ORIGIN
Query Match      97.3%; Score 554.4; DB 10; Length 691;
Best Local Similarity 99.5%; Pred. No. 7,8e-147;
Matches 567; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

Db      326 ATCATCATCTATCTTACTGCGAGATCACAGAGGAGGAAGATTATGATTAAGCTGCTC 385
QY      361 CATGAGCAGATCATTAATATAGGGCAAAAGATAATCTTCCATATGAAAAATTTGATCAG 420
Db      386 CATGAGCAGATCATTAATATAGGGCAAAAGATAATCTTCCATATGAAAAATTTGATCAG 445
QY      421 CTGCAGATATGAGAGAAAGCAAAACCCAGCTCAGTCTGTTCTGGAAAGAGAGAGTG 480
Db      446 CTGCAGATATGAGAGAAAGCAAAACCCAGCTCAGTCTGTTCTGGAAAGAGAGAGTG 505
QY      481 GAGCAACAAGGCTTTTGGATTGGGGGAACATGATGCGATCTTGATCTGGCATCTAGA 540
Db      506 GAGCAACAAGGCTTTTGGATTGGGGGAACATGATGCGATCTTGATCTGGCATCTAGA 565
QY      541 AGATCAGTTCAAGAAAGTAAATCCAAAGGCC 570
Db      566 AGATCAGTTCAAGAAAGTAAATCCAAAGGCC 595

RESULT 4
BG194960
LOCUS      BG194960                768 bp    mRNA    linear    EST 21-APR-2001
DEFINITION RST14018 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG194960
VERSION     BG194960.1  GI:13716535
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 768)
            Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            21227151
            Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scaine@atersys.com
            High quality sequence stop: 469.
FEATURES
    source
        1..768
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Athersys RAGE Library"
            /note="see 'Creation of Genome-wide Protein Expression
            Libraries using Random Activation of Gene Expression',
            Nature Biotechnology, in press. Note that even though the
            cell type indicated is HT1080, since a random activation
            method was used, these sequence tags are not necessarily
            expressed in HT1080 under normal circumstances."
BASE COUNT  197 a      188 c      171 g      212 t
ORIGIN
Query Match      95.4%; Score 543.6; DB 12; Length 768;
Best Local Similarity 98.2%; Pred. No. 9.5e-144;
Matches 560; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

```


Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@ethersys.com
 High quality sequence stop: 537.
 Location/Qualifiers

FEATURES

source

1. 837

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 208 a 209 c 184 g 235 t 1 others
 ORIGIN

Query Match 93.0%; Score 530; DB 12; Length 837;
 Best Local Similarity 97.9%; Pred. No. 7.2e-140;
 Matches 558; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1 ATGATGAATTTCCAGCTCCGAGCAAAAGCGTGGCGGCTCCACAGATGATGACTTTCTTC 60
 DB 124 ATGATGAATTTCCAGCTCCGAGCAAAAGCGTGGCGGCTCCACAGATGATGACTTTCTTC 183
 QY 61 ATCTCTTGCTCTTTTCCATCTTTTCACCGGGGCTTGTGCACCTGGCCATCACCATC 120
 DB 184 ATCTCTTGCTCTTTTCCATCTTTTCACCGGGGCTTGTGCACCTGGTTTTCACCATC 243
 QY 121 TGGAGATTGAAGCTTTCAGCTGCTGCTGCTTTCGAGTGTGCTGCTCTTCATTCAC 180
 DB 244 TGGAGATTGAAGCTTTCAGCTGCTGCTGCTTTCGAGTGTGCTGCTCTTCATTCAC 303
 QY 181 TCCATCTACGCTGATGACACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTTGG 240
 DB 304 TCCATCTACGCTGATGACACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTTGG 363
 QY 241 ATCTATCGCAACCTCATTTGGAAGTGTGCATCTTTTTCATCCTCACCCTCATTTGTCTA 300
 DB 364 ATCTATCGCAACCTCATTTGGAAGTGTGCATCTTTTTCATCCTCACCCTCATTTGTCTA 423
 QY 301 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAAGATATATATAGTGGCTGCTC 360
 DB 424 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAAGATATATATAGTGGCTGCTC 483
 QY 361 CATGAGCAGATCATTAATGAGGCAAAAGATTAATGCTCTGATGAAAAATTTGATCAAG 420
 DB 484 CATGAGCAGATCATTAATGAGGCAAAAGATTAATGCTCTGATGAAAAATTTGATCAAG 543
 QY 421 CTGACAGATATGAGAAAGCAAAACCCAGCTCCTGTTCTGTGAAAAGAGAGAGGTG 480
 DB 544 CTGACAGATATGAGAAAGCAAAACCCAGCTCCTGTTCTGTGAAAAGAGAGAGGTG 603
 QY 481 GAGCAACAAGGCTTTTGGATTTGGGGGAACATGATGAGCTGTGACTTGGATGTATA 540
 DB 604 GAGC-ACAAGGCTTTTGGATTTGGGGGAACATGAGGAG-CTGTGACTTGGATGTATA 661
 QY 541 AGATCAGTTCAAGAAGTATCAAGGCGC 570
 DB 662 AGATCAGTTCAAGAAGTATCAAGGCGC 691

RESULT 7
 BG217267 810 bp mRNA linear EST 21-APR-2001
 LOCUS R3136969 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG217267
 ACCESSION BG217267.1 GI:13743288
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 810)
 REFERENCE
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
 E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
 J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 COMMENT
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@ethersys.com
 High quality sequence stop: 466.
 Location/Qualifiers

FEATURES

1. 810

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 207 a 196 c 180 g 227 t
 ORIGIN

Query Match 91.9%; Score 523.6; DB 12; Length 810;
 Best Local Similarity 96.3%; Pred. No. 4.7e-138;
 Matches 547; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

QY 1 ATGATGAATTTCCAGCTCCGAGCAAAAGCGTGGCGGCTCCACAGATGATGACTTTCTTC 60
 DB 85 ATGATGAATTTCCAGCTCCGAGCAAAAGCGTGGCGGCTCCACAGATGATGACTTTCTTC 144
 QY 61 ATCTCTTGCTCTTTTCCATCTTTTCACCGGGGCTTGTGCACCTGGCCATCACCATC 120
 DB 145 ATCTCTTGCTCTTTTCCATCTTTTCACCGGGGCTTGTGCACCTGGCCATCACCATC 204
 QY 121 TGGAGATTGAAGCTTTCAGCTGCTGCTTTCGAGTGTGCTGCTCTTCATTCAC 180
 DB 205 TGGAGATTGAAGCTTTCAGCTGCTGCTTTCGAGTGTGCTGCTCTTCATTCAC 264
 QY 181 TCCATCTACGCTGATGACACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTTGG 240
 DB 265 TCCATCTACGCTGATGACACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTTGG 324
 QY 241 ATCTATCGCAACCTCATTTGGAAGTGTGCATCTTTTTCATCCTCACCCTCATTTGTCTA 300
 DB 325 ATCTATCGCAACCTCATTTGGAAGTGTGCATCTTTTTCATCCTCACCCTCATTTGTCTA 384
 QY 301 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAAGATATATATAGTGGCTGCTC 360
 DB 385 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAAGATATATATAGTGGCTGCTC 444
 QY 361 CATGAGCAGATCATTAATGAGGCAAAAGATTAATGCTCTGATGAAAAATTTGATCAAG 420
 DB 445 CATGAGCAGATCATTAATGAGGCAAAAGATTAATGCTCTGATGAAAAATTTGATCAAG 504
 QY 421 CTGACAGATATGAGAAAGCAAAACCCAGCTCCTGTTCTGTGAAAAGAGAGAGGTG 480
 DB 505 CTGACAGATATGAGAAAGCAAAACCCAGCTCCTGTTCTGTGAAAAGAGAGAGGTG 564
 QY 481 GAGCAACAAGGCTTTTGGATTT-GGGGGAACATGATGAGCTGTGACTTGGATGTATA 538
 DB 565 GAGCAACAAGGCTTTTGGATTTTGGAGGGAACATGATGAGCTGTGACTTGGATGTATA 624

QY 539 GAAGATCAGTTCAAGAGTAATCCAG 566
|||||
Db 625 GAAATCAATTCAGAGGAAATCCAG 652

RESULT 8
Bg183902 823 bp mRNA linear EST 21-APR-2001
LOCUS R512815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION Bg183902
ACCESSION Bg183902
VERSION Bg183902.1 GI:13705589
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 823)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K., Offenbacher,
J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
2127151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 449.
Location/Qualifiers
1..823
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 211 a 203 c 180 g 229 t
ORIGIN

Query Match 91.9%; Score 523.6; DB 12; Length 823;
Best Local Similarity 97.2%; Pred. No. 4.7e-138;
Matches 554; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 ATGATGAATTTCCAGCTCCGAGGAAGGCTGGGGGCTTCACAGATGACTTTTC 60
|||||
Db 109 ATGATGAATTTCCAGCTCCGAGGAAGGCTGGGGGCTTCACAGATGACTTTTC 168

QY 61 ATCTCTTGCTTTTCCATCTTTCACCGGGGCTTGGACCCGAGCATACATC 120
|||||
Db 169 ATCTCTTGCTTTTCCATCTTTCACCGGGGCTTGGACCCGAGCATACATC 228

QY 121 TGGAGATTGAAGCTTACGCTGAGCTGGCCCTTTTCAGAGTCTGCTCTTCATTCAC 180
|||||
Db 229 TGGAGATTGAAGCTTACGCTGAGCTGGCCCTTTTCAGAGTCTGCTCTTCATTCAC 288

QY 181 TCCATCTACAGCTGGATGACACACCTTAAGTACACGGGCTGACTACGTGGGTTGTTGG 240
|||||
Db 289 TCCATCTACAGCTGGATGACACACCTTAAGTACACGGGCTGACTACGTGGGTTGTTGG 348

QY 241 ATCATGGAACCTCATTTGAAGTGCACCTTTTTCATCTTCACACCTCATTTGCTGA 300
|||||
Db 349 ATCATGGAACCTCATTTGAAGTGCACCTTTTTCATCTTCACACCTCATTTGCTGA 408

QY 301 ATCATCACCCTATCTTTACTGGCAGATGACAGAGGGAAGATTTATGATPAGGCTCTC 360
|||||
Db 409 ATCATCACCCTATCTTTACTGGCAGATGACAGAGGGAAGATTTATGATPAGGCTCTC 468

QY 361 CATGACGATTCATTTATGAGGGCAAGATTAATGTTCTCGATAGAAAATGATCAAG 420
|||||
Db 469 CATGACGATTCATTTATGAGGGCAAGATTAATGTTCTCGATAGAAAATGATCAAG 528

QY 421 CTCGAGATATGAGAGGAAGCAAAACCCAGCTCATCTTGTTCGAAAGAGAGAGGTG 480
|||||
Db 529 CTCGAGATATGAGAGGAAGCAAAACCCAGCTCATCTTGTTCGAAAGAGAGAGGTG 588

QY 481 G-AGCAACAAGGCTTTTGGATTTGGGGGAACATGATGACGATCTTGACATCTAG 539
|||||
Db 589 GAGCAACAAGGCTTTTGGATTTGGGGGAACATGATGACGATCTTGACATCTAG 647

QY 540 AAGATCAGTTCAAGAGATATCCAGGC 569
|||||
Db 648 AATATCAGTTCAAGAGATATCCAGGC 677

RESULT 9
BF375244 698 bp mRNA linear EST 24-NOV-2000
LOCUS BF375244
DEFINITION QV4-ST0212-261199-045-c09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375244
VERSION BF375244.1 GI:11337269
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.R., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&tl=QV4-ST0212-
261199-045-c09&tl=1999-11-26&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 36.
Location/Qualifiers
1..698
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0212"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 177 a 173 c 164 g 184 t
ORIGIN

MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com
 High quality sequence stop: 498.
 Location/Qualifiers
 1..871
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."
 BASE COUNT 252 a 186 c 185 g 246 t
 ORIGIN
 Query Match 77.6%; Score 442.2; DB 12; Length 871;
 Best Local Similarity 99.3%; Pred. No. 7e-115; Indels 0; Gaps 0;
 Matches 444; Conservative 0; Mismatches 3;
 QY 124 AGATTGAGGCTTCAGCTGAGTGGCCCTTTGAGAGTGGCTCTTCATTCACTCC 183
 Db 114 ATTTGAGGCTTCAGCTGAGTGGCCCTTTGAGAGTGGCTCTTCATTCACTCC 173
 QY 184 ATCTACAGCTGATGACACCCCTAAGTACAGGCGCTGCTACCTGGTGGTGGATC 243
 Db 174 ATCTACAGCTGATGACACCCCTAAGTACAGGCGCTGCTACCTGGTGGTGGATC 233
 QY 244 TATCGGAACCTCATTTGGAATGTGCACTTCTTTTCTCTCACTCCATTCGCTAATC 303
 Db 234 TATTTGGAACCTCATTTGGAATGTGCACTTCTTTTCTCTCACTCCATTCGCTAATC 293
 QY 304 ATACACCTATCTTACGTCAGATCACAGAGGAGGAAGATTTAGTATAGGCTGCTCAT 363
 Db 294 ATACACCTATCTTACGTCAGATCACAGAGGAGGAAGATTTAGTATAGGCTGCTCAT 353
 QY 364 GACGACATCTTAATGAGGCGCAAGATTAATATTCCTGATAGAAAAATTTGATCAAGCTG 423
 Db 354 GACGACATCTTAATGAGGCGCAAGATTAATATTCCTGATAGAAAAATTTGATCAAGCTG 413
 QY 424 CAGGATATGAGAGAAAGAAACCCAGCTCACTTGTCTGGAAGAGAGAGTGGAG 483
 Db 414 CAGGATATGAGAGAAAGAAACCCAGCTCACTTGTCTGGAAGAGAGAGTGGAG 473
 QY 484 CACCAAGGCTTTTTCATTTGGGGAAACATGATGGCAGTCTTGATCTGATAGAGA 543
 Db 474 CACCAAGGCTTTTTCATTTGGGGAAACATGATGGCAGTCTTGATCTGATAGAGA 533
 QY 544 TCAGTTCAAGAGGTAATCCAGAGGCC 570
 Db 534 TCAGTTCAAGAGGTAATCCAGAGGCC 560
 RESULT 12
 LOCUS AK016573 2721 bp mRNA linear HRC 19-JAN-2002
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932443J08:homolog to CDNA FLJ13593 FIS, CLONE PLACE1009493, full insert sequence.
 ACCESSION AK016573
 VERSION AK016573.1 GI:12855380
 KEYWORDS HRC; CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
 clone:4932443J08.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiyama, H., Kuenl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, P., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schobach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S., and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE
 AUTHORS 5 (bases 1 to 2721)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arikawa, T., Balderelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haneagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiroaka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama,

BASE COUNT 172 a 193 c 163 g 229 t 1 others
ORIGIN

Query Match 72.2%; Score 411.6; DB 12; Length 758;
Best Local Similarity 96.4%; Pred. No. 3.5e-106;
Matches 453; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

QY 1 ATGATGATTTCCAGCCCTCCGAGCAAGCCGCGGCGCTCAGAGATGACTTTCTTC 60
DB 284 ATGATGATTTCCAGCCCTCCGAGCAAGCCGCGGCGCTCAGAGATGACTTTCTTC 343
QY 61 ATCTCTTCTCTTTTCCCACTTTTCCACGCGGGCTTTTGTGACCCCTGACCATC 120
DB 344 ATCTCTTCTCTTTTCCCACTTTTCCACGCGGGCTTTTGTGACCCCTGACCATC 403
QY 121 TGGAGATTGAAGCCCTCAGCTGAGCTGCGCCCTTTTGTGAGGTCCCTCTTCATTCAC 180
DB 404 TGGAGATTGAAGCCCTCAGCTGAGCTGCGCCCTTTTGTGAGGTCCCTCTTCATTCAC 463
QY 181 TCCATCTACAGCTGGATGACACACCCCTAAGTACAGCGGCTGCTACCTGTGGTTTGG 240
DB 464 TCCATCTACAGCTGGATGACACACCCCTAAGTACAGCGGCTGCTACCTGTGGTTTGG 523
QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGCATCTTTTTCATCTCACCCTCATTTGCTA 300
DB 524 ATCTATCGGAACCTCATTTGGAAGTGTGCATCTTTTTCATCTCACCCTCATTTGCTA 583
QY 301 ATCATTCACCTCTTTTACTGGCAGATCATCAGAGGGAAGATTTATGATTAAGCTGCTC 360
DB 584 ATCATTCACCTCTTTTACTGGCAGATCATCAGAGGGAAGATTTATGATTAAGCTGCTC 643
QY 361 CATGAGCAGATCATTTAATGAGGCAAAAGATTTTCCGTATGAAAAATTTGATCAAG 420
DB 644 C-TTAGCAGATCATTTGAGGCAAAATTAATGTTCCGATGCAATTA-TATCAAG 701
QY 421 CTGCAAGATTTGAGAGAAAGCAAAACCCAGCTGCTCTTCTTGGAAG 470
DB 702 CTGCAAGATTTGAGAGAAAGCAAAACCCAGCT-ACTAGTTCTGGAAG 750

RESULT 14 447 bp mRNA linear EST 12-JUN-2001
LOCUS BG982234/c
DEFINITION C44-CN0089-130201-723-e04 CN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982234
VERSION BG982234.1 GI:14384969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 447)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPBSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=C44&l2=C44-CN0089-130201-723-e04&l3=2001-02-13&l4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 447.
Location/Qualifiers

FEATURES
source
1. 447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1db="CN0089"
/dev_stage="Adult"

/note="Organ: colon,normal; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 114 a 107 c 95 g 131 t
ORIGIN

Query Match 70.4%; Score 401.4; DB 13; Length 447;
Best Local Similarity 99.8%; Pred. No. 2.4e-103;
Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 168 TCTCTTATTCATCTCATCTACAGCTGATGACACCCCTAAGTACAGCGGCTGCTACCT 227
DB 447 TCTCTTATTCATCTCATCTACAGCTGATGACACCCCTAAGTACAGCGGCTGCTACCT 388
QY 228 GTGGGTTGTTGGATCTATCGGAACCTCATTTGGAAGTGTGCATCTTTTTCATCTCCAC 287
DB 387 GTGGGTTGTTGGATCTATCGGAACCTCATTTGGAAGTGTGCATCTTTTTCATCTCCAC 328
QY 288 CCTCATGTGCTATCATCACTCTCTTCTCTGAGATCATCAGAGGGAAGATTAAT 347
DB 327 CCTCATGTGCTATCATCACTCTCTTCTCTGAGATCATCAGAGGGAAGATTAAT 268
QY 348 GATAAGGCTGCTCCATGAGCAGATCATTAATGAGGCAAAAGATTTTCTCTGATAGA 407
DB 267 GATAAGGCTGCTCCATGAGCAGATCATTAATGAGGCAAAAGATTTTCTCTGATAGA 208
QY 408 AAAATTTATCAAGCTGAGATGATGAGAAAGCAAAACCCAGCTGCTTCTGGA 467
DB 207 AAAATTTATCAAGCTGAGATGATGAGAAAGCAAAACCCAGCTGCTTCTGGA 148
QY 468 AAGGAGAGGTGGAGCAAGAGCTTTTTCATTTGGGGAACATGATGAGAGTCTGA 527
DB 147 AAGGAGAGGTGGAGCAAGAGCTTTTTCATTTGGGGAACATGATGAGAGTCTGA 88
QY 528 CTTCGATCTAGAAAGATCAGTTCAAGAGGTAATCCAAAGGCC 570
DB 87 CTTCGATCTAGAAAGATCAGTTCAAGAGGTAATCCAAAGGCC 45

RESULT 15 594 bp mRNA linear EST 24-FEB-2000
LOCUS AM469181/c
DEFINITION hc78f11.x1 NCI-CGAP Gas4 Homo sapiens cDNA clone IMAGE:2898861 3'
ACCESSION AM469181
VERSION AM469181.1 GI:7039287
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 594)
AUTHORS Mammlia; Euthelia; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.illnrl.gov/bbrp/image/image.html

Seq primer: -400p from Glibco

High quality sequence stop: 404.

FEATURES

source

Location/Qualifiers

1..594

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2898861"

/clone_lib="NCI-CGAP_Gas4"

/tissue_type="poorly differentiated adenocarcinoma with

signed ring cell features"

/lab_host="DH10B"

/note="Organ: stomach; Vector: PCMV-SPORT6; Site:1; Salt;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.69 Kb. Life Technologies catalog #:

11549-011"

BASE COUNT 161 a 139 c 108 g 186 t

ORIGIN

Query Match

59.4%; Score 338.8; DB 10; Length 594;

Best Local Similarity 99.4%; Pred. No. 1.7e-85;

Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 229 TGGGTGTTGGATCATCGGAACCTCATTTGGAAGTGCACCTCTTTTCATCCACACC 288
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 594 TGGGTGTTGGATCATCGGAACCTCATTTGGAAGTGCACCTCTTTTCATCCACACC 535

QY 289 CTCATTGTCTAATCATCACTATCTTTACTGCGAGATCACAGAGGAGGAAGATTATG 348
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 534 CTCATTGTCTAATCATCACTATCTTTACTGCGAGATCACAGAGGAGGAAGATTATG 475

QY 349 ATTAAGCTGCTCCATGAGAGATCATTAATGAGGGCAAAAGATTAATGTTCCGTAGTAA 408
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 474 ATTAAGCTGCTCCATGAGAGATCATTAATGAGGGCAAAAGATTAATGTTCCGTAGTAA 415

QY 409 AAATTGATCAAGCTGCAGAGATATGAGAAAGCAAAACCCAGCTCACTTGTCTGGAA 468
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 414 AAATTGATCAAGCTGCAGAGATATGAGAAAGCAAAACCCAGCTCACTTGTCTGGAA 355

QY 469 AGGAGAGAGGTGAGCAACAGGCTTTTTCATTTGGGGAAACATGATGAGAGCTTTGAC 528
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 354 AGGAGAGAGGTGAGCAACAGGCTTTTTCATTTGGGGAAACATGATGAGAGCTTTGAC 295

QY 529 TTGCGATCTAGAAAGATCAAGTTCAGAAAGGTAAATCCAAAGGCC 570
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db 294 TTGCGATCTAGAAAGATCAAGTTCAGAAAGGTAAATCCAAAGGCC 253

```

Search completed: November 9, 2002, 03:15:54
Job time : 2224 secs

THIS PAGE BLANK (USPTO)